

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 13:07:57 ; Search time 2039.32 Seconds  
(without alignments)  
12788.784 Million cell updates/sec

Title: US-09-784-340-1  
Perfect score: 2759

Sequence: 1 caaccatgcagatcagtg.....ctgcagccgtctacgtacgc 2759

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 10228115 seqs, 4726426750 residues

Word size : 0

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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ESP:*
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257: gb_est188:*
258: gb_est189:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



**AUTHORS** Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,D., Young,D., Zhao,S., Adams,M.D. and Hood,L.

**TITLE** Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

**JOURNAL MEDLINE** Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

**COMMENT** Contact: Mahairas GG, Wallace JC, Hood L. High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@edong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 634 row: D column: 24 Seq primer: SP6 Class: BAC ends High quality sequence stop: 446.

**FEATURES** Location/Qualifiers

source 1..446

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="Plate-634 Col-24 Row-D"

/clone\_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

**BASE COUNT** 143 a 87 c 63 g 151 t 2 others

**ORIGIN**

Query Match 9.4%; Score 259; DB 228; Length 446; Best Local Similarity 100.0%; Pred. No. 1.4e-116; Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1806 gtgtctactctctctctactctgtgacacagacagatgaatctcaattttccta 1865  
 DB 72 ggtcttactctctctctctactcttttgacacagacatgaattactttaaattttcccta 131  
 QY 1866 ttcttgatatacctgtttccatgacgtcatttctcttaaccttaagtataggttgc 1925  
 DB 132 ttcttgatattcactgtttccatgacgtcatttctcttaaccttaagtataggttgc 191  
 QY 1926 ctgcaatatagtcgtattctcgtgtttgcaacacacatgagttaagaagtaaaaatg 1985  
 DB 192 ctgcaatatagtcgtattctcgtgtttgcaacacacatgagttaagaagtaaaaatg 251  
 QY 1986 taaatcacaacaaattcagtaaacacacacaaatgaagattcagacattagctt 2045  
 DB 252 taaatcacaacaaattcagtaaacacacacacaaatgaagattcagacattagctt 311  
 QY 2046 gttatgagtacaataatga 2064  
 DB 312 gttatgagtacaataatga 330

**RESULT** 3

LOCUS BG249053 671 bp mRNA EST 13-FEB-2001  
 DEFINITION 602361828P1 NIH\_MGC\_89 Homo sapiens cDNA clone IMAGE:4470199 5', mRNA sequence.  
 ACCESSION BG249053  
 VERSION BG249053.1 GI:12758669  
 KEYWORDS EST.

**SOURCE** human.

**ORGANISM** Homo sapiens

**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 671)

**AUTHORS** NIH-MGC http://mgi.nci.nih.gov/.

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)

**JOURNAL** Unpublished (1999)

**COMMENT** Contact: Robert Strausberg, Ph.D. Email: cga@bbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM10287 row: h column: 08 High quality sequence stop: 661.

**FEATURES** Location/Qualifiers

source 1..671

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4470199"

/clone\_lib="NIH\_MGC\_89"

/tissue\_type="hypernephroma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: Kidney; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

**BASE COUNT** 206 a 123 c 153 g 189 t

**ORIGIN**

Query Match 9.1%; Score 252; DB 175; Length 671; Best Local Similarity 100.0%; Pred. No. 4e-113; Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 ttgttgacctagctctgaatgtcttgcaggttcaacacgtgcaatcagttataaat 365  
 DB 109 ttgttgacctagctctgaatgtcttgcaggttcaacacgtgcaatcagttataaat 168  
 QY 366 taaatgatttttttttgtaataaagaagaactttaaatagtgtgagagcttattct 425  
 DB 169 taaatgatttttttttgtaataaagaagaactttaaatagtgtgagagcttattct 228  
 QY 426 acaatcagacgttcttgaaagaagctcaagaaacacactagatgattatgcttagacc 485  
 DB 229 acaatcagacgttcttgaaagaagctcaagaaacacactagatgattatgcttagacc 288  
 QY 486 ctgtgattcccttgtagaagctgtagtgcgttgcaggtccctttgtgtcacac 545  
 DB 289 ctgtgattcccttgtagaagctgtagtgcgttgcaggtccctttgtgtgtcacac 348  
 QY 546 ttagaattctcg 557  
 DB 349 ttagaattctcg 360

**RESULT** 4

LOCUS BG402144 898 bp mRNA EST 12-MAR-2001  
 DEFINITION 602465689P1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4593694 5', mRNA sequence.  
 ACCESSION BG402144  
 VERSION BG402144.1 GI:13295592  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

REFERENCE
AUTHORS      1 (bases 1 to 898)
TITLE        NIH-MGC http://mgc.nci.nih.gov/
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: Clontech Laboratories, Inc.
              cDNA Library Preparation: Clontech Laboratories, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.lnl.gov
              Plate: LICM134 row: a column: 23
              High quality sequence stop: 557.

FEATURES
Source
1. 898
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:4593694"
   /lab_host="NIH-MGC-75"
   /lab_host="DH10B (T1 phage-resistant)"
   /note="Organ: Kidney; Vector: pDNR-LIB (Clontech); site_1:
   SfiI (ggcgctcgcc); site_2: SfiI (ggcattatggcc); 5' and
   3' adaptors were used in cloning as follows: 5' adaptor
   sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor sequence:
   5'-ATTCTAGAGCCGAGGCGCCGACATG-dT(30)BN-3' (where B = A,
   C, or G and N = A, C, G, or T). Average insert size 1.65
   kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
   by PCR. This library was enriched for full-length clones
   and was constructed by Clontech Laboratories (Palo Alto,
   CA). Note: this is a NIH-MGC Library."

BASE COUNT      249 a      175 c      165 g      309 t
ORIGIN

Query Match      8.5%; Score 234; DB 153; Length 898;
Best Local Similarity 99.6%; Pred. No. 3.2e-104;
Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 gtatgtggttcctgcgtgacctgtgtgcaactgtatattctgtccacaatgtttc 1567
DB 1 ggtgattgggttcctgcgtgacctgtgtgcaactgtatattctgtccacaatgtttc 60

QY 1568 ttatttcctgtcaaaaatttaaaactagaagaagatagaagaggaatagatttt 1627
DB 61 ttattttcctgtcaaaaatttaaaactagaagaagatagaagaggaatagatttt 120

QY 1628 ccaaatcaagaagaacctatggtggaatcctgttaattccaccacataagatttgc 1687
DB 121 ccaaatcaagaagaacctatggtggaatcctgttaattccaccacataagatttgc 180

QY 1688 gaaaacctgcatattcattatatactatctcgttatttatttactttagctatagcctag 1747
DB 181 gaaaacctgcatattcattatatactatctcgttatttatttactttagctatagcctag 240

QY 1748 aattcctatgcatgaggtgtgtgatatctcattcttcttcgttg 1792
DB 241 aattcctatgcatgaggtgtgtgatatctcattcttcttcgttg 285

RESULT 5
LOCUS      AO165734      367 bp      DNA      GSS      16-OCT-1998
DEFINITION HS_3065_B1_H05_MR_C1T Approved Human Genomic Sperm Library D Homo
ACCESSION  AO165734.1 GI:3563929
VERSION     AO165734.1
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE
AUTHORS      1 (bases 1 to 367)
TITLE        Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
JOURNAL      Kellar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
MEDLINE      Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT      Sequence-tagged connectors: A sequence approach to mapping and
              scanning the human genome
              Contact: Mahairas GG, Wallace JC, Hood L
              High Throughput Sequencing Center
              University of Washington
              401 Queen Anne Avenue North, Seattle, WA 98109, USA
              Tel: (206) 616-3618
              Fax: (206) 616-3887
              Email: jwallace@u.washington.edu
              Sequence Tagged Connector
              Plate: 3065 row: P column: 9
              Class: BAC ends
              High quality sequence stop: 367.

FEATURES
Source
1. 367
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="plate=3065 Col=9 Row=P"
   /clone_lib="CIT Approved Human Genomic Sperm Library D"
   /sex="male"
   /note="Organ: sperm; Vector: pBel0BAC11; BAC Clones in
   E-Coli DH10B"

BASE COUNT      113 a      74 c      50 g      130 t
ORIGIN

Query Match      8.3%; Score 229; DB 225; Length 367;
Best Local Similarity 99.6%; Pred. No. 9e-102;
Matches 279; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 atttctcagtggtgcttaactctctctcctcactgtgtgacacagagacatgaatc 1853
DB 42 atttctcagtggtgcttaactctctctcctcactgtgtgacacagagacatgaatc 101

QY 1854 taaatttcctattcctgatactactgttccacgaagctattctctcactcctaactga 1913
DB 102 taaatttcctattcctgatactactgttccacgaagctattctctcactcctaactga 161

QY 1914 tgataggtgacccgtcaaatgctgattcctggtgtgttgacacacacatgagatgaag 1973
DB 162 tgataggtgacccgtcaaatgctgattcctggtgtgttgacacacacatgagatgaag 221

QY 1974 aagtaaaaaatgtaaaattcacaattcagtaaacacacacacaaatgaagatccta 2033
DB 222 aagtaaaaaatgtaaaattcacaattcagtaaacacacacacacaaatgaagatccta 281

QY 2034 tgacattagcttgatagagtaacataagatttctctc 2073
DB 282 tgacattagcttgatagagtaacataagatttctctc 321

RESULT 6
LOCUS      AO784447      595 bp      DNA      GSS      03-AUG-1999
DEFINITION HS_3141_A2_H04_T7C CIT Approved Human Genomic Sperm Library D Homo
ACCESSION  AO784447
VERSION     AO784447.1 GI:5692071
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 595)
AUTHORS    Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Kellar,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.

```

**TITLE** Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
**JOURNAL** Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
**MEDLINE** 99380589  
**COMMENT** Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones may be purchased from Research Genetics (info@resgen.com).  
 BAC end Web Server: <http://www.htsc.washington.edu>  
 Plate: 3141 row: 0 column: 8  
 Seq primer: 17  
 Class: BAC ends  
 High quality sequence stop: 595.  
 Location/Qualifiers

**FEATURES**  
 source  
 1..595  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate-3141 Col-8 Row=0"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /sex="male"  
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

**BASE COUNT** 186 a 115 c 87 g 200 t 7 others  
**ORIGIN**

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e-90;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1868 tctgatatactggttccatgacgtcattctcttaaccttaagtataggtgacct 1927  
 |||||||  
 DB 133 tctgatatactggttccatgacgtcattctcttaaccttaagtataggtgacct 192  
 |||||||  
 QY 1928 gcaatgctgcttctgctgtttgcacacacacatgagtgtaaaagaataaaatgta 1987  
 |||||||  
 DB 193 gcaatgctgcttctgctgtttgcacacacacatgagtgtaaaagaataaaatgta 252  
 |||||||  
 QY 1988 aaattcacaaaattcagtaaacacacacaaatcaatgaagcattctatgacattgct 2047  
 |||||||  
 DB 253 aaattcacaaaattcagtaaacacacacaaatcaatgaagcattctatgacattgct 312  
 |||||||  
 QY 2048 tatgagtaacataatgattttctt 2073  
 |||||||  
 DB 313 tatgagtaacataatgattttctt 338  
 |||||||

**RESULT** 7  
**LOCUS** B80712 444 bp DNA GSS 24-OCT-1998  
**DEFINITION** CIT-HSP-2050M23.TF CIT-HSP Homo sapiens genomic clone 2050M23, DNA sequence.  
**ACCESSION** B80712  
**VERSION** B80712.1 GI:2867735  
**KEYWORDS** GSS.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 444)  
 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.  
 Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)  
**TITLE** Unpublished (1998)  
**JOURNAL** Other\_GSS: CIT-HSP-2050M23.TF  
**COMMENT** Contact: Mark Adams  
 Department of Eukaryotic Genomics

The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mddams@tigr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html)  
 Seq primer: M13-21  
 Class: BAC ends.  
 Location/Qualifiers

**FEATURES**  
 source  
 1..444  
 /organism="Homo sapiens"  
 /db\_xref="GDB:7056698"  
 /db\_xref="taxon:9606"  
 /clone="2050M23"  
 /clone\_lib="CIT-HSP"  
 /sex="male"  
 /cell\_type="Sperm"  
 /note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2: HindIII"

**BASE COUNT** 124 a 110 c 71 g 139 t  
**ORIGIN**

Query Match  
 Best Local Similarity 100.0%; Pred. No. 1.1e-66;  
 Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1342 ttataaagaagatgctatagattatcaagaattcaccatatacaacctgtaagccct 1401  
 |||||||  
 DB 287 ttatgaagagatgctatagattatcaagaattcaccatatacaacctgtaagccct 346  
 |||||||  
 QY 1402 agatgagcagctctcttgatcaggttgcacgcacaaaggagccagcactg 1461  
 |||||||  
 DB 347 agatgagcagctctcttgatcaggttgcacgcacaaaggagccagcactg 406  
 |||||||  
 QY 1462 atcagctgccatgacactgctgcttcacagcact 1499  
 |||||||  
 DB 407 atcagctgccatgacactgctgcttcacagcact 414  
 |||||||

**RESULT** 8  
**LOCUS** A0728754/c 474 bp DNA GSS 15-JUL-1999  
**DEFINITION** HS\_5462\_B1\_E10\_Sp6E RPCT-11 Human Male BAC Library Homo sapiens genomic clone Plate=1038 Col=19 Row=0, DNA sequence.  
**ACCESSION** A0728754  
**VERSION** A0728754.1 GI:5500306  
**KEYWORDS** GSS.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** 1 (bases 1 to 474)  
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
**TITLE** Contact: Mahairas GG, Wallace JC, Hood L  
**JOURNAL** High Throughput Sequencing Center  
**MEDLINE** 99380589  
**COMMENT** Contact: Mahairas GG, Wallace JC, Hood L  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))

or from Resear h Genetics (info@resgen.com). BAC end Web Server:  
<http://www.htsc.washington.edu>  
 Plate: 1038 row: J column: 19  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 474.  
 Location/Qualifiers

## FEATURES

source

1. 474  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate-1038 Col-19 Row-J"  
 /clone\_lib="RPCI-11 Human Male BAC Library"  
 /sex="male"  
 /note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACe3.6 vector at EcoRI sites"  
 BASE COUNT 146 a 90 c 90 g 143 t 5 others  
 ORIGIN

Query Match 5.1%; Score 142; DB 232; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-59;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1588 taataaacagagaagataagagagagatagatcttcacaaattcagaagaagactg 1647  
 |||  
 Db 159 TAAATAAAGCTAGAAAGATGAGAAAGAGGGAATCTTCCAAATTCAGAAAGACCTG 100

QY 1648 atggggtaactcgttaattccagccacatagaaattgtgtgaaacctgtatttcac 1707  
 |||  
 Db 99 ATGGGTAATCCGTGAATTCAGCCACATAGATTGTGGAAGAACTCTGCTATTTCAT 40

QY 1708 attactatctgtatttat 1729  
 |||  
 Db 39 ATTATCTATCTCTTATTTTAT 18

## RESULT 9

LOCUS AO371717/c 601 bp DNA GSS 20-MAY-1999  
 DEFINITION RPEC11-155J15.TV RPEC1-11 Homo sapiens genomic clone RPEC1-11-155J15,  
 DNA sequence.  
 ACCESSION AO371717  
 VERSION AO371717.1 GI:4342740  
 KEYWORDS GSS.

## SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 601)  
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter  
 J.C.

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Use of BAC End Sequences from Library RPEC1-11 for Sequence-Ready  
 Map Building  
 Unpublished (1997)  
 Other\_GSSs: RPEC11-155J15.TV  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPEC1-11. For BAC  
 library availability, please contact Pter de Jong  
 (pter@edj.med.buflalo.edu). Clones may be purchased from  
 BACBAC Resources (<http://bacpac.med.buflalo.edu/ordering>) or from  
 Research Genetics (info@resgen.com). BAC end search page:  
[http://www.tigr.org/cdb/humgen/Bac\\_end\\_search/Bac\\_end\\_search.html](http://www.tigr.org/cdb/humgen/Bac_end_search/Bac_end_search.html)  
 Seq primer: 17  
 Class: BAC ends.

FEATURES  
 Location/Qualifiers

source

1. 601  
 /organism="Homo sapiens"  
 /db\_xref="GDB:7559366"  
 /db\_xref="taxon:9606"  
 /clone="RPCI-11-155J15"  
 /clone\_lib="RPCI-11"  
 /sex="Male"  
 /cell\_type="lymphocytes"  
 /note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 RPEC11 Human Male BAC Library"  
 BASE COUNT 227 a 89 c 85 g 200 t  
 ORIGIN

Query Match 4.8%; Score 132; DB 227; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-54;  
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 tatgacagactaacagacagatgacctcttggaagaagataaaatcaatgcttc 681  
 |||  
 Db 553 TATGACAGACTAAGACAGATGACCTTCTGGAAGATAAAATCAATGCTTTC 494

QY 682 agttgttccactctgtgattcagattacgactatcatcttgggaagatttag 741  
 |||  
 Db 493 AGTTTCTTCACCTCTGATTCAGATTCAGACTATCATTTTGGGAAGATTTTATAG 434

QY 742 taaggcattagg 753  
 |||  
 Db 433 TAAGGCATTAGG 422

## RESULT 10

LOCUS AM301261/c 536 bp mRNA EST 18-JAN-2000  
 DEFINITION xs69g08.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2774942 3',  
 mRNA sequence.  
 ACCESSION AM301261  
 VERSION AM301261.1 GI:6710938  
 KEYWORDS EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 536)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

## JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgaps@remail.nih.gov  
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
[www.bio.lnl.gov/bdrp/image/image.html](http://www.bio.lnl.gov/bdrp/image/image.html)  
 Seq primer: -40UP from GIBCO  
 High quality sequence stop: 461.  
 Location/Qualifiers

## FEATURES

source

1. 536  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2774942"  
 /clone\_lib="NCI\_CGAP\_Kid11"  
 /lab\_host="DH10B"  
 /note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Plasmid DNA from the normalized library NCI\_CGAP\_Kid3 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 132376-132391, 145607-145675, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 214 a 62 c 52 g 208 t

Query Match 3.2%; Score 88; DB 114; Length 536;  
Best Local Similarity 100.0%; Pred. No. 3.9e-32;  
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2449 aaatgatgaatactcataatcttctctataatcaaaagataattactgtaga 2508  
|||||  
DB 518 AAATGATGAACTCATATCTTCTCTAATCAAGATTAATTACTGTAGAAA 459

QY 2509 aataagagatgctgttcttgaaagtaa 2536  
|||||  
DB 458 AATAAGAGATGCTGTCTGAAAGTAA 431

RESULT 11  
AI816782 552 bp mRNA EST 21-DEC-1999  
LOCUS wj3a11.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA IMAGE:2404700 3',  
DEFINITION mRNA sequence.  
ACCESSION AI816782  
VERSION AI816782.1 GI:5435861  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 552)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tumor Gene Index  
Tumor Gene Index  
Unpublished (1997)  
CONTACT: Robert Strausberg, Ph.D.  
Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdrrp/image/image.html  
Insert length: 1622 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 450.  
Location/Qualifiers

FEATURES  
source  
1..552  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2404700"  
/clone\_lib="NCI\_CGAP\_Kid12"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: p7T73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Kid5 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(clonoids 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 215 a 65 c 52 g 220 t

Query Match 3.2%; Score 88; DB 102; Length 552;  
Best Local Similarity 100.0%; Pred. No. 3.9e-32;  
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2449 aaatgatgaatactcataatcttctctataatcaaaagataattactgtaga 2508  
|||||  
DB 527 AAATGATGAACTCATATCTTCTCTAATCAAGATTAATTACTGTAGAAA 468

QY 2509 aataagagatgctgttcttgaaagtaa 2536  
|||||  
DB 467 AATAAGAGATGCTGTCTGAAAGTAA 440

RESULT 12  
AM771510 498 bp mRNA EST 04-MAY-2000  
LOCUS hu57e11.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:3032012 3',  
DEFINITION mRNA sequence.  
ACCESSION AM771510  
VERSION AM771510.1 GI:7703567  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 498)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tumor Gene Index  
Tumor Gene Index  
Unpublished (1997)  
CONTACT: Robert Strausberg, Ph.D.  
Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 459.  
Location/Qualifiers

FEATURES  
source  
1..498  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3032012"  
/clone\_lib="NCI\_CGAP\_Kid11"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: p7T73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Kid3 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(clonoids 132376-132391, 145607-145675, and  
1500552-1502855). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 191 a 58 c 50 g 199 t

Query Match 3.2%; Score 87; DB 120; Length 498;  
Best Local Similarity 100.0%; Pred. No. 1.2e-31;  
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2450 aaatgatgaatactcataatcttctctataatcaaaagataattactgtaga 2509  
|||||  
DB 498 AAATGATGAACTCATATCTTCTCTAATCAAGATTAATTACTGTAGAAA 439

QY 2510 aataagagatgctgttcttgaaagtaa 2536



Db 438 ATAAAGATGCTTGTCTGAAGTAA 412

RESULT 13  
LOCUS A1670866/c 518 bp mRNA EST 16-DEC-1999  
DEFINITION wa05b11.x1 NCI-CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:229727 3',  
MRA sequence.  
ACCESSION A1670866  
VERSION A1670866.1 GI:4850597  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 518)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@email.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html  
Insert Length: 1265 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 457.  
Location/Qualifiers  
1. 518  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:229727"  
/clone\_1ib="NCI-CGAP\_Kid11"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: pT730-Pac (Pharmacia) with  
a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
Plasmid DNA from the normalized library NCI-CGAP Kid3  
purification, and as circles were made in vitro. Following HAP  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneids 1322376-1323911, 1456007-1456775, and  
1500552-1502855). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 203 a 61 c 54 g 200 t

ORIGIN

Query Match 3.1%; Score 85; DB 23; Length 518;  
Best Local Similarity 100.0%; Pred. No. 1.2e-30;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2452 atgataaatacataattctatctcacaacaaagataaattactgtgaanaat 2511  
|||||  
Db 518 ATGATGATACATCATATCTTATCTCTATTAATCAAAAGATATATTACTGTGAANAAT 459  
QY 2512 aaagagatgctgttcttgaagtaa 2536  
|||||  
Db 458 AAAGAGATGCTGTCTGAAGTAA 434

RESULT 14  
LOCUS BF132129 538 bp mRNA EST 24-OCT-2000  
DEFINITION 601821157F1 NIH\_MGC\_58 Homo sapiens cDNA clone IMAGE:4052654 5',  
MRA sequence.

ACCESSION BF132129  
VERSION BF132129.1 GI:10971169  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 538)  
AUTHORS NIH-MGC http://imgc.ncbi.nlm.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@email.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM890 row: b column: 15  
High quality sequence stop: 536.  
Location/Qualifiers  
1. 538  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4052654"  
/clone\_1ib="NIH\_MGC\_58"  
/tissue\_type="hypernephroma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: Kidney; Vector: pNIR-LIB (Clontech); Site.1:  
SfiI (ggcgccctggcc); Site.2: SfiI (ggccatattggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-ATTCTAGAGGCGGAGCGCGGCGACATG-dt(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 172 a 103 c 118 g 145 t

ORIGIN

Query Match 2.6%; Score 73; DB 144; Length 538;  
Best Local Similarity 100.0%; Pred. No. 1e-24;  
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1062 catccataggagccaactcggctgctatgattgatacccgagaatgactcttg 1121  
|||||  
Db 450 CATCCACATTAGAGCCAAATACGCTGATATATGGAATCCCAAGATGATCTCTTG 509  
QY 1122 gtcatcccaaac 1134  
|||||  
Db 510 GTCATCCCAAAAC 522

RESULT 15  
LOCUS AQ438194 552 bp DNA GSS 31-MAR-1999  
DEFINITION HS.5083.B2.E12.T7A RPCI-11 Human Male BAC Library Homo sapiens  
genomic clone Plate-659 Col-24 Row-J, DNA sequence.  
ACCESSION AQ438194  
VERSION AQ438194.1 GI:4549533  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 552)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCT-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
 or from Research Genetics (info@resgen.com). BAC end Web Server:  
<http://www.htsc.washington.edu>  
 Plate: 659 row: J column: 24

Class: BAC ends  
 Seq primer: T7  
 High quality sequence stop: 552.

#### FEATURES

source location/Qualifiers  
 1..552  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate=659 Col=24 Row=J"  
 /clone\_lib="RPCT-11 Human Male BAC Library"  
 /sex="male"  
 /note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACe3.6 vector at EcoRI sites"  
 BASE COUNT 172 a 111 c 84 g 181 t 4 others  
 ORIGIN

Query Match 2.6%; Score 72; DB 228; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-24;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2071 |tttcaatttaataagcccttaccatccccagcattctgactcagacaatgaatt 2130  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
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QY 2131 |gctaaaaatgac 2142  
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 DB 393 GCTAAAAATGAC 404

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